Amendments to the Claims/Listing of Claims

Please amend claims 14, 19 and 31 as follows. This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Withdrawn) A composition comprising the ligand binding domain of a farnesoid X receptor (FXR) in crystalline form.

2. (Withdrawn) A composition according to claim 1 further comprising a ligand of said FXR.

3. (Withdrawn) A composition according to claim 2, wherein said ligand is selected from the group consisting of fexaramine, fexarine, fexarene and GW4064.

4.-5. Cancelled.

6. (Withdrawn) A composition according to claim 1 as described by the structure coordinates set forth in Appendix 1, or a portion thereof sufficient to define the points of interaction between said ligand binding domain and a ligand therefor.

7. (Withdrawn) A composition according to claim 2 as described by the structure coordinates set forth in Appendix 1, or a portion thereof sufficient to define the points of interaction between said ligand binding domain and said ligand.

8. (Withdrawn) A composition according to claim 2, wherein the crystals belong to space group $P2_12_12_1$ with unit cell dimensions of about:

a = 37 Å, b = 57 Å, c = 117 Å,

$\alpha = 90°$, $\beta = 90°$, and $\gamma = 90°$.

9. Cancelled.

10. (Withdrawn) A composition according to claim 1, wherein said ligand binding domain comprises amino acid residues 248 – 476 of SEQ ID NO:1.

11. (Withdrawn) A computer for producing a three-dimensional representation of a farnesoid X receptor (FXR) molecule or molecular complex or a homologue of said FXR molecule or molecular complex, wherein said FXR molecule or molecular complex or a homologue of said FXR molecule or molecular complex comprises a ligand binding domain defined by structure coordinates obtained from X-ray diffraction data obtained from crystals of said FXR molecule or molecular complex or a homologue of said FXR molecule or molecular complex, said computer comprising:

(i) a computer-readable data storage medium comprising a data storage material encoded with computer-readable data, wherein said data comprises X-ray diffraction data obtained from crystals of said FXR molecule or molecular complex or a homologue of said FXR molecule or molecular complex;

(ii) a working memory for storing instructions for processing said computer-readable data;

(iii) a central-processing unit coupled to said working memory and to said computer-readable data storage medium for processing said computer-machine readable data into said three-dimensional representation; and

(iv) a display coupled to said central-processing unit for displaying said three-dimensional representation.

12. (Withdrawn) A computer according to claim 11, wherein said structure coordinates are set forth in Appendix 1, or a portion thereof sufficient to define the points of interaction between said ligand binding domain and a ligand therefor.

13. (Withdrawn) A computer for determining at least a portion of the structure coordinates corresponding to X-ray diffraction data obtained from a farnesoid X receptor (FXR) molecule or molecular complex or a homologue of said FXR molecule or molecular complex, said computer comprising:

(i) a computer-readable data storage medium comprising a data storage material encoded with computer-readable data, wherein said data comprises at least a portion of the structure coordinates of Appendix 1;

(ii) a computer-readable data storage medium comprising a data storage material encoded with computer-readable data, wherein said data comprises X-ray diffraction data obtained from said FXR molecule or molecular complex or a homologue of said FXR molecule or molecular complex;

(iii) a working memory for storing instructions for processing said computer-readable data of (i) and (ii);

(iv) a central-processing unit coupled to said working memory and to said computer-readable data storage medium of (i) and (ii) for performing a Fourier transform of the machine readable data of (i) and for processing said computer-readable data of (ii) into structure coordinates; and

(v) a display coupled to said central-processing unit for displaying said structure coordinates of said FXR molecule or molecular complex.

14. (Currently amended) A method of ~~predicting a~~ **screening** molecules **to determine those which are** capable of binding to a farnesoid X receptor (FXR) molecule, said method comprising:

modeling a test molecule that potentially interacts with a ~~composition comprising the~~ ligand binding domain of a farnesoid X receptor (FXR) ~~in crystalline form~~ **comprising amino acid residues 248 - 476 of SEQ ID NO:1**,

wherein said ligand binding domain is defined by a plurality of structure coordinates of the ligand binding domain of a FXR molecule or a fragment thereof, **and**

wherein said structure coordinates are ~~derived from~~ **based on** X-ray diffraction data obtained from crystals of said FXR molecule or molecular complex, or a homologue of said FXR molecule or molecular complex,

whereby those compounds which lack repulsive electrostatic interaction with FXR molecule in their bound state are capable of binding to a farnesoid X receptor (FXR) molecule therefor.

15. (Original) A method according to claim 14, wherein said plurality of structure coordinates are set forth in Appendix 1, or a portion thereof sufficient to define the points of interaction between said ligand binding domain and a ligand therefor.

16.-17. Cancelled.

18. (Original) A method according to claim 14, wherein said test molecule is developed using a computer algorithm to predict a three-dimensional representation of said test molecule interacting with a FXR based upon a three-dimensional representation of a FXR molecule or fragment thereof.

19. (Currently amended) A method of ~~identifying a~~ **screening** compound**s to determine those** with agonist, partial agonist, or antagonist activity with respect to a farnesoid X receptor (FXR) molecule, said method comprising:

(a) modeling a test compound that potentially interacts with ~~the~~ **a** ligand binding domain of ~~said~~ **a** FXR molecule ~~or a fragment thereof~~ **comprising amino acid residues 248 – 476 of SEQ ID NO:1**,

wherein said ligand binding domain is defined by a plurality of structure coordinates of a crystalline form of the ligand binding domain of a FXR molecule or a fragment thereof, **and**

wherein said plurality of structure coordinates are ~~derived from~~ **based on** X-ray diffraction data obtained from crystals of said FXR molecule or

molecular complex, or a homologue of said FXR molecule or molecular complex; and

(b) determining the ability of said test compound to modulate the activity of said FXR molecule in the optional presence of a known FXR agonist,

whereby those molecules which bind and alter the activity of farnesoid X receptor (FXR) molecule are identified as agonists or partial agonists, and those compounds which bind but do not alter the activity of farnesoid X receptor (FXR) molecule are identified as antagonists therefor.

20. (Original) A method according to claim 19, wherein said plurality of structure coordinates are set forth in Appendix 1, or a portion thereof sufficient to define the points of interaction between said ligand binding domain and a ligand therefor.

21. (Withdrawn) A compound identified by the method of claim 19.

22. (Withdrawn) A pharmaceutical composition comprising a compound identified by the method of claim 19 and a pharmaceutically acceptable carrier therefor.

23.-30. Cancelled.

31. (Withdrawn; currently amended) A method for determining whether a test compound is capable of binding to the ligand binding domain of a farnesoid X receptor (FXR) molecule **comprising amino acid residues 248 - 476 of SEQ ID NO:1**, said method comprising:

(a) determining the points of interaction between a crystalline form of the ligand binding domain of a FXR, and one or more known ligand(s) therefor; and

(b) analyzing said test compound to determine whether similar points of interaction exist between said test compound and said ligand binding domain.

32. (Withdrawn) A method according to claim 31, wherein step (a) utilizes a plurality of structure coordinates derived from X-ray diffraction data obtained from crystals of said FXR molecule or molecular complex or a homologue of said FXR molecule or molecular complex to define said points of interaction.

33. (Withdrawn) A method according to claim 32, wherein said structure coordinates are set forth in Appendix 1, or a portion thereof sufficient to define the points of interaction between said ligand binding domain and said ligand(s).

34.-37. Cancelled.